



131

## SEQUENCE LISTING

<110> NICKlin, Martin  
Barton, Jenny

<120> IL-1L1 GENE AND POLYPEPTIDE PRODUCTS

<130> MSA-021.01

<140> 09/617,720

<141> 2000-07-17

<160> 54

<170> PatentIn Ver. 2.1

<210> 1

<211> 2563

<212> DNA

<213> Homo sapiens

<400> 1  
aggggagtct acaccctgtg gagctcaaga tggtccttag tggggcgctg tgcttccgaa 60  
tgaaggactc ggcattgaag gtgtttatc tgcataataa ccagctcta gctggagggc 120  
tgcatgcagg gaaggcatt aaaggtgaag agatcagcgt ggccccat cggtggctgg 180  
atgccacgcgt gtcccccgcc atccctgggtg tccagggtgg aagccagtgc ctgtcatgtg 240  
gggtggggca ggagccgact ctaacactag agccagtgaa catcatggag ctctatctt 300  
gtgccaagga atccaagagc ttcacctct accggcgaaa catggggctc acctccagct 360  
tcgagtcggc tgcctaccgg ggctgggtcc tgcacgggt geetgaagcc gatcagcctg 420  
tcagactcac ccagcttccc gagaatgggtg gctggaatgc cccatcaca gacttctact 480  
tccagcagtg tgacttagggc aacgtgc(cc) cccagaactc cctggcaga gccagctcg 540  
gtgagggggtg agtggaggag acccatgggg gacaatact ctttctgtc tcaggacccc 600  
cagggtctgac ttagtggca cctgaccact ttgtcttctg gttcccaatt tgcataaatt 660  
ctgagatttg gagctcagtc cagggtcctc cccactggg tggtgcact gctgtggAAC 720  
cttgtaaaaaa ccatgtgggg taaactgggataaacatgaa aagatttctg tgggggtggg 780  
gtgggggagt gctggaaatc attcctgttt aatggtaact gacaagtgtt accctgagcc 840  
cccgaggcca acccatcccc agttggacct tataagggtca gtagctctcc acatgaagtc 900  
ctctcactca ccactgtgca ggagaggagg gtggtcataag agtcaggat ctatggccct 960  
tggcccagcc ccacccccc ttcccttatcc tgcactgtc atatgttacc tttcttatct 1020  
cttcctcat catctgttg tgggcatggag gaggtggta tgcagaaga aatggttcga 1080  
gctcagaaga taaaagataa gttaggtatg ctgatccct tttaaaacc caagatacaa 1140  
tcaaaatccc agatgctggt ctctattccc atgaaaaagt gctcatgaca tattgagaag 1200  
acctacttac aaagtggcat atattgcaat ttattttat taaaagatac ctattttat 1260  
atttctttat agaaaaaaagt ctggaagagt ttacttcaat tgttagcaatg tcagggtgt 1320  
ggcagtatag gtgattttc ttttaattct gttaattttat ctgtatttcc taattttct 1380  
acaatgaaga tgaatttcctt gtataaaaat aagaaaaagaa attaatctt aggttaagcag 1440  
agcagacatc atctctgatt gtcctcagcc tccaaatccc cagagtaat tcaaattgaa 1500  
tcgagctctg ctgctctgg tgggtgtat agtgcattgg aaacagatct cagaaagcc 1560  
actgaggagg aggctgtgt gagtttgggt ggctggaaat tctgggtaaag gaacttaaag 1620  
aacaatccc atctgttac tctttccctt aaggatcaca gcccctgggaa ttccaaggca 1680  
ttggatccag tctctaagaa ggctgctgtt ctgggtgtat tgcgtcccc tcaaattcac 1740  
atccttcttgc gaatctcgt ctgtgagtt atttggagat aaggtctctg cagatgtat 1800  
tagttaagac aaggtcatgc tggatgaagg tagacctaaa ttcaatatga ctggtttct 1860  
tgtatgaaaa ggagaggaca cagagacaga ggagacgcgg ggaagactat gtaaagatga 1920  
aggcagagat cggagtttg cagccacaag ctaagaaaca ccaaggattt gggcaaccat 1980  
cagaagcttg gaagaggcaa agaagaattt ttccttagag gcttttagagg gataacggct 2040  
ctgctgaaac cttaatctca gacttccagc ctccctgaacg aagaaagaat aaatttcggc 2100  
tggtaaagc caccaaggat aattggttac agcagctcta gggaaactaat acagctgcta 2160

aaatgatccc tgcctccatc tgtttacatt ctgtgtgtgt cccctccac aatgtaccaa 2220  
 agttgtcttt gtgacccaat agaatatggc agaagtgatg gcatgcact tcgaagatta 2280  
 ggttataaaa gacactgcag ctctacttg agccctctct ctctgcacc caccggcccc 2340  
 aatcttatctt ggctcaactcg ctctggggga agctagctgc catgctatga gcaggcctat 2400  
 aaagagactt acgtggtaaa aatgaagtc tcctgcccac agccacatta gtgaacctag 2460  
 aagcagagac tctgtgagat aatcgatgtt tggtttta agttgctcag tttggctca 2520  
 acttgttatg cagcaataga taaataatat gcagagaaag aga 2563

<210> 2  
 <211> 39  
 <212> DNA  
 <213> Homo sapiens

<400> 2  
 ttgaggaaca ggcagactcc acagctcccg ccaggagaa

39

<210> 3  
 <211> 42  
 <212> DNA  
 <213> Homo sapiens

<400> 3  
 aaggaaggag ggagaaggga aggagtgaag gaaggagtga aa

42

<210> 4  
 <211> 1284  
 <212> DNA  
 <213> Murine sp.

<400> 4  
 ggcacgaggg gagcctgctt tctacttagg tctcaaattt tccagccttg tctttgccta 60  
 aaatttcctg ctgttattt caaaataggg tctacatact gtggagctca tgatggttct 120  
 gagtggggca ctatgcttcc gaatgaagga ttcaagccttg aaggtactgt atctgcacaa 180  
 taaccagctg ctggctggag gactgcacgc agagaaggc attaaagggtg aggagatcag 240  
 tgttgtccca aatcgggcac tggatgcac tctgtccct gtcatcctgg gcggtcaagg 300  
 aggaagccag tgcctatctt gtggacaga gaaaggccaa attctgaaac ttgagccagt 360  
 gaacatcatg gagctctacc tcggggccaa ggaatcaaag agcttcaccc tctaccggcg 420  
 ggatatgggt cttacctcca gcttcgaatc cgctgcctac ccaggctggt tccctctgcac 480  
 ctcaccggaa gctgaccagc ctgtcaggct cactcagatc cctgaggacc cggcctggga 540  
 tgctccatc acagacttct actttcagca gtgtgacttag ggctgcgtgg tccccaaaaac 600  
 tccataagca gaggcagagt aggcaactggc ggctcctgtat agaggataga gagacagagg 660  
 agctccacag tagtggctt actcctctcc ttccctactg gactcccgct tctgacctaa 720  
 ggcacacaga cactctttc tcctgcattc cagtgcgtgt aaatcttctg gtatttggag 780  
 ctcaatgtgt agattcttc agattggatg gtactacctc tggtgtggaa cccaatagaa 840  
 accacgtagg accaacaataag agcaacataa aagattcttg ggtgaagaag aggtggaaac 900  
 tgttcataca tagtaagatc tgacacagta cctcagaagt cctgcattc ttatgttct 960  
 ggagaaaatg gaggggggggt caccaagact ttctctggct ggctggcccc ttccctcaa 1020  
 cctttctgac atctgcagcc tctctcatc ttgccttcat tctctggcccc tgaaccgaga 1080  
 ggggtgatatc aggatagctg acagaagatg accaggcaca ctgtcctggt ttgaaaccag 1140  
 aggggacaat aaaaaaccct gattctggtc tctactcaca taaaaagaag cttgtgaaca 1200  
 ttaagtggga agagattgct actaaataac atacctgtta atttcatctt aattaaaata 1260  
 tacttctcta tattatataat ttta 1284

133

<210> 5  
<211> 155  
<212> PRT  
<213> Homo sapiens

<400> 5  
Met Val Leu Ser Gly Ala Leu Cys Phe Arg Met Lys Asp Ser Ala Leu  
1 5 10 15  
  
Lys Val Leu Tyr Leu His Asn Asn Gln Leu Leu Ala Gly Gly Leu His  
20 25 30  
  
Ala Gly Lys Val Ile Lys Gly Glu Glu Ile Ser Val Val Pro Asn Arg  
35 40 45  
  
Trp Leu Asp Ala Ser Leu Ser Pro Val Ile Leu Gly Val Gln Gly Gly  
50 55 60  
  
Ser Gln Cys Leu Ser Cys Gly Val Gly Gln Glu Pro Thr Leu Thr Leu  
65 70 75 80  
  
Glu Pro Val Asn Ile Met Glu Leu Tyr Leu Gly Ala Lys Glu Ser Lys  
85 90 95  
  
Ser Phe Thr Phe Tyr Arg Arg Asp Met Gly Leu Thr Ser Ser Phe Glu  
100 105 110  
  
Ser Ala Ala Tyr Pro Gly Trp Phe Leu Cys Thr Val Pro Glu Ala Asp  
115 120 125  
  
Gln Pro Val Arg Leu Thr Gln Leu Pro Glu Asn Gly Gly Trp Asn Ala  
130 135 140  
  
Pro Ile Thr Asp Phe Tyr Phe Gln Gln Cys Asp  
145 150 155

<210> 6  
<211> 155  
<212> PRT  
<213> Murine sp.

<400> 6  
Met Val Leu Ser Gly Ala Leu Cys Phe Arg Met Lys Asp Ser Ala Leu  
1 5 10 15  
  
Lys Val Leu Tyr Leu His Asn Asn Gln Leu Leu Ala Gly Gly Leu His  
20 25 30  
  
Ala Glu Lys Val Ile Lys Gly Glu Glu Ile Ser Val Val Pro Asn Arg  
35 40 45  
  
Ala Leu Asp Ala Ser Leu Ser Pro Val Ile Leu Gly Val Gln Gly Gly  
50 55 60  
  
Ser Gln Cys Leu Ser Cys Gly Thr Glu Lys Gly Pro Ile Leu Lys Leu  
65 70 75 80

134  
4

Glu Pro Val Asn Ile Met Glu Leu Tyr Leu Gly Ala Lys Glu Ser Lys  
85 90 95

Ser Phe Thr Phe Tyr Arg Arg Asp Met Gly Leu Thr Ser Ser Phe Glu  
100 105 110

Ser Ala Ala Tyr Pro Gly Trp Phe Leu Cys Thr Ser Pro Glu Ala Asp  
115 120 125

Gln Pro Val Arg Leu Thr Gln Ile Pro Glu Asp Pro Ala Trp Asp Ala  
130 135 140

Pro Ile Thr Asp Phe Tyr Phe Gln Gln Cys Asp  
145 150 155

<210> 7

<211> 141

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus  
polypeptide sequence

<400> 7

Met Val Leu Ser Gly Ala Leu Cys Phe Arg Met Lys Asp Ser Ala Leu  
1 5 10 15

Lys Val Leu Tyr Leu His Asn Asn Gln Leu Leu Ala Gly Gly Leu His  
20 25 30

Ala Lys Val Ile Lys Gly Glu Glu Ile Ser Val Val Pro Asn Arg Leu  
35 40 45

Asp Ala Ser Leu Ser Pro Val Ile Leu Gly Val Gln Gly Gly Ser Gln  
50 55 60

Cys Leu Ser Cys Gly Pro Leu Leu Glu Pro Val Asn Ile Met Glu Leu  
65 70 75 80

Tyr Leu Gly Ala Lys Glu Ser Lys Ser Phe Thr Phe Tyr Arg Arg Asp  
85 90 95

Met Gly Leu Thr Ser Ser Phe Glu Ser Ala Ala Tyr Pro Gly Trp Phe  
100 105 110

Leu Cys Thr Pro Glu Ala Asp Gln Pro Val Arg Leu Thr Gln Pro Glu  
115 120 125

Trp Ala Pro Ile Thr Asp Phe Tyr Phe Gln Gln Cys Asp  
130 135 140

<210> 8

<211> 138

<212> PRT

<213> Homo sapiens

135

<400> 8  
Phe Arg Ile Trp Asp Val Asn Gln Lys Thr Phe Tyr Leu Arg Asn Asn  
1 5 10 15  
  
Gln Leu Val Ala Gly Tyr Leu Gln Gly Pro Asn Val Asn Leu Glu Glu  
20 25 30  
  
Lys Ile Asp Val Val Pro Ile Glu Pro His Ala Leu Phe Leu Gly Ile  
35 40 45  
  
His Gly Gly Lys Met Cys Leu Ser Cys Val Lys Ser Gly Asp Glu Thr  
50 55 60  
  
Arg Leu Gln Leu Glu Ala Val Asn Ile Thr Asp Leu Ser Glu Asn Arg  
65 70 75 80  
  
Lys Gln Asp Lys Arg Phe Ala Phe Ile Arg Ser Asp Ser Gly Pro Thr  
85 90 95  
  
Thr Ser Phe Glu Ser Ala Ala Cys Pro Gly Trp Phe Leu Cys Thr Ala  
100 105 110  
  
Met Glu Ala Asp Gln Pro Val Ser Leu Thr Asn Met Pro Asp Glu Gly  
115 120 125  
  
Val Met Val Thr Lys Phe Tyr Phe Gln Glu  
130 135

<210> 9  
<211> 73  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Consensus  
polypeptide sequence

<400> 9  
Phe Arg Asp Lys Tyr Leu Asn Asn Gln Leu Ala Gly Leu Val Glu Ile  
1 5 10 15  
  
Val Val Pro Pro Leu Gly Gly Cys Leu Ser Cys Gly Glu Leu Leu  
20 25 30  
  
Glu Val Asn Ile Leu Lys Lys Phe Phe Arg Asp Gly Thr Ser Phe Glu  
35 40 45  
  
Ser Ala Ala Pro Gly Trp Phe Leu Cys Thr Glu Ala Asp Gln Pro Val  
50 55 60  
  
Leu Thr Pro Gly Thr Phe Tyr Phe Gln  
65 70

<210> 10  
<211> 465

<212> DNA  
<213> Homo sapiens

<400> 10  
atggtcctga gtggggcgct gtgcttccga atgaaggact cggcattgaa ggtgctttat 60  
ctgcataata accagcttct agctggaggg ctgcacgcag ggaaggcat taaaggtgaa 120  
gagatcagcg tggccccaa tcggtggtg gatgccagcc tgtccccgt catcctgggt 180  
gtccagggtg gaagccagtg cctgtcatgt ggggtggggc aggagccgac tctaacaacta 240  
gagccagtga acatcatgga gctctatctt ggtccaagg aatccaagag cttcaccttc 300  
taccggcggg acatgggct cacctccagc ttcgagtcgg ctgcctaccc gggctggttc 360  
ctgtgcacgg tgcctgaagc cgatcaggct gtcagactca cccagcttcc cgagaatgg 420  
ggctggaaatg ccccatcac agacttctac ttccagcagt gtgac 465

<210> 11  
<211> 465  
<212> DNA  
<213> Murine sp.

<400> 11  
atggttctga gtggggcact atgcttccga atgaaggatt cagcctgaa ggtactgtat 60  
ctgcacaata accagctgct ggctggagga ctgcacgcag agaaggcat taaaggtgag 120  
gagatcagtg ttgtcccaa tcgggcactg gatgccagtc tgtccccgt catcctggc 180  
gtcaaggag gaagccagtg cctatctgt gggacagaga aaggccaat tctgaaaactt 240  
gagccagtga acatcatgga gctctaccc gggccaagg aatcaaagag cttcaccttc 300  
taccggcggg atatgggtct tacctccagc ttcaaatccg ctgcctaccc aggctggttc 360  
ctctgcacct caccggaagc tgaccagcct gtcaggctca ctcagatccc tgaggacccc 420  
gcctggatg ctccatcac agacttctac ttccagcagt gtgac 465

<210> 12  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Conserved  
consensus DNA sequence

<220>  
<221> modified\_base  
<222> (1)..(41)  
<223> "n" represent a variable base

<400> 12  
acaatnaaaa nccngatnc tggctctan tcncatnaaa a

41

<210> 13  
<211> 155  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Recombinant  
IBR polypeptide

<400> 13  
 Met Val Leu Ser Gly Ala Leu Cys Phe Arg Met Lys Asp Ser Ala Leu  
 1 5 10 15  
 Lys Val Leu Tyr Leu His Asn Asn Gln Leu Leu Ala Gly Gly Leu His  
 20 25 30  
 Ala Gly Lys Val Ile Lys Gly Glu Glu Ile Ser Val Val Pro Asn Arg  
 35 40 45  
 Trp Leu Asp Ala Ser Leu Ser Pro Val Ile Leu Gly Val Gln Gly Gly  
 50 55 60  
 Ser Gln Cys Leu Ser Cys Gly Val Gly Gln Glu Pro Thr Leu Thr Leu  
 65 70 75 80  
 Glu Pro Val Asn Ile Met Glu Leu Tyr Leu Gly Ala Lys Glu Ser Lys  
 85 90 95  
 Ser Phe Thr Phe Tyr Arg Arg Asp Met Gly Leu Thr Ser Ser Phe Glu  
 100 105 110  
 Ser Ala Ala Tyr Pro Gly Trp Phe Leu Cys Thr Val Pro Glu Ala Asp  
 115 120 125  
 Gln Pro Val Arg Leu Thr Gln Leu Pro Glu Asn Gly Gly Trp Asn Ala  
 130 135 140  
 Pro Ile Thr Asp Phe Tyr Phe Gln Gln Cys Asp  
 145 150 155

<210> 14  
<211> 154  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Recombinant  
IBR polypeptide

<400> 14  
Val Leu Ser Gly Ala Leu Cys Phe Arg Met Lys Asp Ser Ala Leu Lys  
1 5 10 15  
Val Leu Tyr Leu His Asn Asn Gln Leu Leu Ala Gly Gly Leu His Ala  
20 25 30  
Gly Lys Val Ile Lys Gly Glu Glu Ile Ser Val Val Pro Asn Arg Trp  
35 40 45  
Leu Asp Ala Ser Leu Ser Pro Val Ile Leu Gly Val Gln Gly Gly Ser  
50 55 60  
Gln Cys Leu Ser Cys Gly Val Gly Gln Glu Pro Thr Leu Thr Leu Glu  
65 70 75 80

138  
8

Pro Val Asn Ile Met Glu Leu Tyr Leu Gly Ala Lys Glu Ser Lys Ser  
85 90 95

Phe Thr Phe Tyr Arg Arg Asp Met Gly Leu Thr Ser Ser Phe Glu Ser  
100 105 110

Ala Ala Tyr Pro Gly Trp Phe Leu Cys Thr Val Pro Glu Ala Asp Gln  
115 120 125

Pro Val Arg Leu Thr Gln Leu Pro Glu Asn Gly Gly Trp Asn Ala Pro  
130 135 140

Ile Thr Asp Phe Tyr Phe Gln Gln Cys Asp  
145 150

<210> 15

<211> 157

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Recombinant  
IBR polypeptide

<400> 15

Gly Ser Ser Val Leu Ser Gly Ala Leu Cys Phe Arg Met Lys Asp Ser  
1 5 10 15

Ala Leu Lys Val Leu Tyr Leu His Asn Asn Gln Leu Leu Ala Gly Gly  
20 25 30

Leu His Ala Gly Lys Val Ile Lys Gly Glu Glu Ile Ser Val Val Pro  
35 40 45

Asn Arg Trp Leu Asp Ala Ser Leu Ser Pro Val Ile Leu Gly Val Gln  
50 55 60

Gly Gly Ser Gln Cys Leu Ser Cys Gly Val Gly Gln Glu Pro Thr Leu  
65 70 75 80

Thr Leu Glu Pro Val Asn Ile Met Glu Leu Tyr Leu Gly Ala Lys Glu  
85 90 95

Ser Lys Ser Phe Thr Phe Tyr Arg Arg Asp Met Gly Leu Thr Ser Ser  
100 105 110

Phe Glu Ser Ala Ala Tyr Pro Gly Trp Phe Leu Cys Thr Val Pro Glu  
115 120 125

Ala Asp Gln Pro Val Arg Leu Thr Gln Leu Pro Glu Asn Gly Gly Trp  
130 135 140

Asn Ala Pro Ile Thr Asp Phe Tyr Phe Gln Gln Cys Asp  
145 150 155

a

139  
9

<210> 16  
<211> 73  
<212> DNA  
<213> Homo sapiens

<400> 16  
ctggcaatgg caggcagggaa agacagagga aggaaggagg gagaagggaa ggagtgaagg 60  
aaggagtgaa aaa 73

<210> 17  
<211> 16  
<212> PRT  
<213> Homo sapiens

<400> 17  
Met Ala Gly Arg Lys Asp Arg Gly Arg Lys Glu Gly Glu Gly Lys Glu  
1 5 10 15

<210> 18  
<211> 54  
<212> DNA  
<213> Homo sapiens

<400> 18  
ttggagggAAC aggcagactc cacagctccc gccaggagaa aggaacattc tgag 54

<210> 19  
<211> 10  
<212> DNA  
<213> Homo sapiens

<400> 19  
tccaaaatacg 10

<210> 20  
<211> 10  
<212> DNA  
<213> Homo sapiens

<400> 20  
gatgttcag 10

<210> 21  
<211> 10  
<212> DNA  
<213> Homo sapiens

<400> 21  
tttccccacag 10

<210> 22  
<211> 10

a

140  
10

<212> DNA  
<213> Homo sapiens

<400> 22  
ctgccggcag

10

<210> 23  
<211> 10  
<212> DNA  
<213> Homo sapiens

<400> 23  
ctggcaatgg

10

<210> 24  
<211> 10  
<212> DNA  
<213> Homo sapiens

<400> 24  
ttggaggaac

10

<210> 25  
<211> 10  
<212> DNA  
<213> Homo sapiens

<400> 25  
gggagtctac

10

<210> 26  
<211> 10  
<212> DNA  
<213> Homo sapiens

<400> 26  
aatgaaggac

10

<210> 27  
<211> 10  
<212> DNA  
<213> Homo sapiens

<400> 27  
gtgaagagat

10

<210> 28  
<211> 10  
<212> DNA  
<213> Homo sapiens

<400> 28

*141*  
*xx*

ccagtgaaca

10

<210> 29  
<211> 10  
<212> DNA  
<213> Homo sapiens

<400> 29  
agtggaaaaag

10

<210> 30  
<211> 10  
<212> DNA  
<213> Homo sapiens

<400> 30  
acattctgag

10

<210> 31  
<211> 10  
<212> DNA  
<213> Homo sapiens

<400> 31  
tgtgcttccg

10

<210> 32  
<211> 10  
<212> DNA  
<213> Homo sapiens

<400> 32  
gtcattaaag

10

<210> 33  
<211> 10  
<212> DNA  
<213> Homo sapiens

<400> 33  
aacactagag

10

<210> 34  
<211> 10  
<212> DNA  
<213> Homo sapiens

<400> 34  
agagaaaagag

10

<210> 35

*a* 142  
12

<211> 10  
<212> DNA  
<213> Homo sapiens

<400> 35  
gtaaggaaga

10

<210> 36  
<211> 10  
<212> DNA  
<213> Homo sapiens

<400> 36  
gtatgctctg

10

<210> 37  
<211> 10  
<212> DNA  
<213> Homo sapiens

<400> 37  
gtgagtgtat

10

<210> 38  
<211> 10  
<212> DNA  
<213> Homo sapiens

<400> 38  
gttgggtatg

10

<210> 39  
<211> 10  
<212> DNA  
<213> Homo sapiens

<400> 39  
gtgagacttg

10

<210> 40  
<211> 10  
<212> DNA  
<213> Homo sapiens

<400> 40  
aaacaaaatgc

10

<210> 41  
<211> 104  
<212> PRT  
<213> Homo sapiens

143

<400> 41  
Met Val Leu Ser Gly Ala Leu Cys Phe Arg Met Lys Asp Ser Ala Leu  
1 5 10 15  
  
Lys Val Leu Tyr Leu His Asn Asn Gln Leu Leu Ala Gly Gly Leu His  
20 25 30  
  
Ala Gly Lys Val Ile Lys Gly Glu Glu Ile Ser Val Val Pro Asn Arg  
35 40 45  
  
Trp Leu Asp Ala Ser Leu Ser Pro Val Ile Leu Gly Val Gln Gly Gly  
50 55 60  
  
Ser Gln Cys Leu Ser Cys Gly Val Gly Gln Glu Pro Thr Leu Thr Leu  
65 70 75 80  
  
Glu Val Asn Ile Met Glu Leu Tyr Leu Gly Ala Lys Glu Ser Lys Ser  
85 90 95  
  
Phe Thr Phe Tyr Arg Arg Asp Met  
100

<210> 42  
<211> 100  
<212> PRT  
<213> Homo sapiens

<400> 42  
Arg Lys Ser Ser Lys Met Gln Ala Phe Arg Ile Trp Asp Val Asn Gln  
1 5 10 15  
  
Lys Thr Phe Tyr Leu Arg Asn Asn Gln Leu Val Ala Gly Tyr Leu Gln  
20 25 30  
  
Gly Pro Asn Val Asn Leu Glu Glu Lys Ile Asp Val Val Pro Ile Glu  
35 40 45  
  
Pro His Ala Leu Phe Leu Gly Ile His Gly Gly Lys Met Cys Leu Ser  
50 55 60  
  
Cys Val Lys Ser Gly Asp Glu Thr Arg Leu Gln Leu Glu Val Asn Ile  
65 70 75 80  
  
Thr Asp Leu Ser Glu Asn Arg Lys Gln Asp Lys Arg Phe Ala Phe Ile  
85 90 95  
  
Arg Ser Asp Ser  
100

<210> 43  
<211> 6540  
<212> DNA  
<213> Homo sapiens

<400> 43  
catgagcaaa gatgttaata caaagatgtt tgtcacaaca tggtttcaa tagcaaaaaa 60

agagagaaaa atatataaaa gacaaataac agtggatagg tttcaataaa taatgttaca 120  
gtgatacagt taaatactat acagctattg aagcatgtca ttattcatat ttagtatgga 180  
aagatattt gctatttgc tacatgaaaa aatgagggttg gaaaaagtat aggtttgtg 240  
aatctgtgt atgaaagctg tctatagttt catgtgtatg tgtgtggagg aaaaagtgtt 300  
gtcattgggt ttctgtatgactcagaa aagacaagta ttcacatTT ttcttggtggc 360  
tgcattggat ttccaggtt ttctacaatg aacatgttagg ctgaacattc cctaagcagg 420  
agagtcccac ctctaacatc tcctgttaggc ctggcaatgg caggcaggaa agacagagga 480  
aggaaggagg gagaaggaa ggagtgaagg aaggagtgaa aaagtaagg aagaaaggaa 540  
atagggagg aagggaggaa atgggaaaggaa aagaaaggaa aggaaggaaa gagggaggaa 600  
agaaaggaag ggaaaaggaa gggagttagt gaatgaaaaga tggaaaagaa gaagaaaggaa 660  
agggaggcag ggaggaaaga aagttgcgt tcccttgc tgccatggc actgacttt 720  
agggtctgaa agcccctgag atgaaaagc ctatgtctca caaagagctg gaaagcctca 780  
aggaagttt tcaatattt tggaaaggaaa ctgtctccag aagctccct ccccacgaca 840  
gataatgagc agcaagtgc tctggcact taggtgtatg taaaatcagc ctggaaatcc 900  
tgctccctcct caggtcctgg cagtttcagg gcccctccctt aggccttact taaaaggctg 960  
aggcatcctt ggaggaaacag gcagactcca cagtcctccgc caggagaaag gaacattctg 1020  
agttatgtctc tggggcgctg gtgttacgg agtctctcc tgaccctcaga cccagaatct 1080  
gtccgtgga ggctgttac atgctgggaa gctcggtgca gctgcttgc ccccgacacc 1140  
cagccaaactc agcctcttc tccatgattt tctttgttt attccaaaat aggggagtt 1200  
acaccctgtg gagctcaaga tggctctgag tggggcgctg tgctccgtt gagtgtatga 1260  
ggccctgggt tgggtgggtc ctccggagga agtgagttt ggttagaccc gttgtccagc 1320  
tctgagcagg agggaggaag ggaggggtcg ccattgcagc tggaaattt tgaccagcac 1380  
ctcattgtctc ttaggtttt ccacgcctt ttccaaatagg ggcaggactg gggcaggcca 1440  
tctcacaagg ggtccctgtat gctgaggggg acaagtgaac ctcacgtct agagctccag 1500  
ccaagtctat ccaaggtggg aacgggggcc aggtccctg ctcagagctc cgccattgtc 1560  
ccccatcaca gtgaatggat gtaagctcac ccactctgtg cccctaccc cctgtactc 1620  
tttggggata ataataaaaac aaaaccattt accatcagcc agtctgtcca cccactggca 1680  
tgtaccaagc cagacactct gccgtgttct gggcttaaca acagaggatg agagtggtc 1740  
tttctctcag tctaataaaag cacttccac gatgtttct atgggactcg attagaggag 1800  
tcccacagag gcatccagga gatgtttac acagtggagc tctctgtatca agtaaatgca 1860  
ggaaattctg ctttctacat cctctctaa gagaaccaca gcccagctca gcatatgagt 1920  
gactgaggtt ttctgaagta aggcaactt gttaatcgta ttttagctatg catcgaccca 1980  
attttacac tgcattccctt tcccccataa aacttttggaa gaaaccact tttaggataca 2040  
tcttccacct cataggatgc caggaaatca actgagttca aagatgagaa acaactttga 2100  
aaagttaaat aaaagaaatt taaattttaa gaaactcctc acttagtaag gaatataatga 2160  
ccaaatagaa atacatgtat cttgaagaat tgaagaatca ggcttaacg tggaagaggc 2220  
ctggatgtta tccaaaccat catcttagt tagcaatggg gaggctcagg cccagagtg 2280  
gcgagagagt tgcattctgc gactcagcag cattggaggc atagatgggg caagaaccta 2340  
gggctctgac tcaccgtgca gcttcttctc caacaggaga tgggttgggg cagaaaaggt 2400  
tgaatagggtt gaaggagcaa accacagact ccagtgggg actgtggggt catcctccct 2460  
gtagggcatg agcccagcag ggctgggaga caaggctgtg ctgttacttc tggcacagta 2520  
ggaagaaaga gagacaaaat gcctgagatc agggggttct ctggatccag ggcattgtgg 2580  
agtgtccacc ctcctccataa tgcattctc accccttctt gatgtttcag aatgaaggac 2640  
tcggcattga aggtgtttt tctgcataat aaccagcttc tagctggagg gtcgtatgca 2700  
gggaaggtca ttaaagggtt gtgtgaaac atgacccact ttccttggtc tctataact 2760  
ctcaggggag gggcctgaa gagggcttag aatagtctata cagattagca taggcctaca 2820  
gagcccagggc attagggcag cacaaccat gctctaagca aaggcaataaa aataactaca 2880  
cctctcagca aagtgaagac acacgctctg gggccacctg aagcttctgt gcagaagtga 2940  
gaatgttttcaagaggctt gtctgtcat tcccttacag gtatgtttt gtcacggatt 3000  
gcattccctg ggagccagta agtaccaagg agagaactaa cgtatgttctt ctataccctt 3060  
tttccctat gggagttgtt ttctgcctt ccaccctggg tcccctctgc tctctgaaga 3120  
tcctcagtc ctttagagtgg agggaccatc agaacaggtt gcatgttgg acctctgtct 3180  
tgctcactt gccccatgca ctgcaacagg tccctctcta aaatagttt cacctgccc 3240  
cctggggcac cttgctgag cacatgtcc aggttagatcc ttcagctagg ccatatgtgt 3300  
atgtgtgtgc ttactgggt atgtatgtt gcatgtcaggc atatatgtt gaggcatatgt 3360  
gtgcattgtat gatctgtat gtaaccatgt atgtgttagt gcaggtatgt aggtatgagc 3420  
atgtgtgtgtt atatgtat gttgtcatgc atgtatgtt gcatgtatgtt atctgtatgt 3480  
tgtgggtgtt gagggatgtt acagagaccc ttttgcctt cagcaaccc 3540

145

<210> 44  
<211> 152  
<212> PRT  
<213> *Homo sapiens*

*146*  
~~16~~

<400> 44  
Arg Pro Ser Gly Arg Lys Ser Ser Lys Met Gln Ala Phe Arg Ile Trp  
1 5 10 15  
  
Asp Val Asn Gln Lys Thr Phe Tyr Leu Arg Asn Asn Gln Leu Val Ala  
20 25 30  
  
Gly Tyr Leu Gln Gly Pro Asn Val Asn Leu Glu Glu Lys Ile Asp Val  
35 40 45  
  
Val Pro Ile Glu Pro His Ala Leu Phe Leu Gly Ile His Gly Gly Lys  
50 55 60  
  
Met Cys Leu Ser Cys Val Lys Ser Gly Asp Glu Thr Arg Leu Gln Leu  
65 70 75 80  
  
Glu Ala Val Asn Ile Thr Asp Leu Ser Glu Asn Arg Lys Gln Asp Lys  
85 90 95  
  
Arg Phe Ala Phe Ile Arg Ser Asp Ser Gly Pro Thr Thr Ser Phe Glu  
100 105 110  
  
Ser Ala Ala Cys Pro Gly Trp Phe Leu Cys Thr Ala Met Glu Ala Asp  
115 120 125  
  
Gln Pro Val Ser Leu Thr Asn Met Pro Asp Glu Gly Val Met Val Thr  
130 135 140  
  
Lys Phe Tyr Phe Gln Glu Asp Glu  
145 150

<210> 45  
<211> 153  
<212> PRT  
<213> Homo sapiens

<400> 45  
Ala Pro Val Arg Ser Leu Asn Cys Thr Leu Arg Asp Ser Gln Gln Lys  
1 5 10 15  
  
Ser Leu Val Met Ser Gly Pro Tyr Glu Leu Lys Ala Leu His Leu Gln  
20 25 30  
  
Gly Gln Asp Met Glu Gln Gln Val Val Phe Ser Met Ser Phe Val Gln  
35 40 45  
  
Gly Glu Glu Ser Asn Asp Lys Ile Pro Val Ala Leu Gly Leu Lys Glu  
50 55 60  
  
Lys Asn Leu Tyr Leu Ser Cys Val Leu Lys Asp Asp Lys Pro Thr Leu  
65 70 75 80  
  
Gln Leu Glu Ser Val Asp Pro Lys Asn Tyr Pro Lys Lys Met Glu  
85 90 95  
  
Lys Arg Phe Val Phe Asn Lys Ile Glu Ile Asn Asn Lys Leu Glu Phe  
100 105 110

147

Glu Ser Ala Gln Phe Pro Asn Trp Tyr Ile Ser Thr Ser Gln Ala Glu  
115 120 125

Asn Met Pro Val Phe Leu Gly Gly Thr Lys Gly Gly Gln Asp Ile Thr  
130 135 140

Asp Phe Thr Met Gln Phe Val Ser Ser  
145 150

<210> 46  
<211> 159  
<212> PRT  
<213> Homo sapiens

<400> 46  
Ser Ala Pro Phe Ser Phe Leu Ser Asn Val Lys Tyr Asn Phe Met Arg  
1 5 10 15

Ile Ile Lys Tyr Glu Phe Ile Leu Asn Asp Ala Leu Asn Gln Ser Ile  
20 25 30

Ile Arg Ala Asn Asp Gln Tyr Leu Thr Ala Ala Leu His Asn Leu  
35 40 45

Asp Glu Ala Val Lys Phe Asp Met Gly Ala Tyr Lys Ser Ser Lys Asp  
50 55 60

Asp Ala Lys Ile Thr Val Ile Leu Arg Ile Ser Lys Thr Gln Leu Tyr  
65 70 75 80

Val Thr Ala Gln Asp Glu Asp Gln Pro Val Leu Leu Lys Glu Met Pro  
85 90 95

Glu Ile Pro Lys Thr Ile Thr Gly Ser Glu Thr Asn Leu Leu Phe Phe  
100 105 110

Trp Glu Thr His Gly Thr Lys Asn Tyr Phe Thr Ser Val Ala His Pro  
115 120 125

Asn Leu Phe Ile Ala Thr Lys Gln Asp Tyr Trp Val Cys Leu Ala Gly  
130 135 140

Gly Pro Pro Ser Ile Thr Asp Phe Gln Ile Leu Glu Asn Gln Ala  
145 150 155

<210> 47  
<211> 157  
<212> PRT  
<213> Homo sapiens

<400> 47  
Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile Arg Asn Leu Asn  
1 5 10 15

*148*  
*18*

Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro Leu Phe Glu Asp  
20 25 30

Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg Thr Ile Phe Ile  
35 40 45

Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met Ala Val Thr Ile  
50 55 60

Ser Val Lys Cys Glu Lys Ile Ser Thr Leu Ser Cys Glu Asn Lys Ile  
65 70 75 80

Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile Lys Asp Thr Lys  
85 90 95

Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asn Lys  
100 105 110

Met Gln Phe Glu Ser Ser Tyr Glu Gly Tyr Phe Leu Ala Cys Glu  
115 120 125

Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys Glu Asp Glu Leu  
130 135 140

Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu Asp  
145 150 155

<210> 48

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus  
peptide sequence

<220>

<221> MOD\_RES

<222> (1)..(6)

<223> Xaa represents a variable amino acid

<400> 48

Leu Lys Xaa Leu Xaa Leu

1 5

<210> 49

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus  
peptide sequence

<220>

<221> MOD\_RES

149  
x9

<222> (1)..(7)  
<223> Xaa represents a variable amino acid

<400> 49  
Ile Thr Asp Phe Xaa Xaa Gln  
1 5

<210> 50  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Consensus  
peptide sequence

<220>  
<221> MOD\_RES  
<222> (1)..(12)  
<223> Xaa represents a variable amino acid

<400> 50  
Tyr Leu Xaa Asn Asn Gln Leu Xaa Ala Gly Xaa Leu  
1 5 10

<210> 51  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Consensus  
peptide sequence

<220>  
<221> MOD\_RES  
<222> (1)..(9)  
<223> Xaa represents a variable amino acid

<400> 51  
Leu Glu Xaa Val Asn Ile Xaa Xaa Leu  
1 5

<210> 52  
<211> 24  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Consensus  
peptide sequence

<220>  
<221> MOD\_RES  
<222> (1)..(24)

*a*

*150*  
*20*

<223> Xaa represents a variable amino acid

<400> 52

Thr Xaa Ser Phe Glu Ser Ala Ala Xaa Pro Gly Trp Phe Leu Cys Thr  
1 5 10 15

Xaa Xaa Glu Ala Asp Gln Pro Val  
20

<210> 53

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Binding domain

<400> 53

Phe Gly Phe Arg  
1

*but*  
*C1*

<210> 54

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: N-terminal  
extension

<400> 54

Gly Ser Ser Gly Leu Arg Arg Ala Ser Leu Gly Ser Ser  
1 5 10